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<210> SEQ ID NO 17
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer
<400> SEQUENCE: 17

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<210> SEQ ID NO 18
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer
<400> SEQUENCE: 18

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<210> SEQ ID NO 19
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Sequence of the locus specific for buccal epithelial cells after bisulfite treatment assuming 100% unmethylation of all CpG sites
<400> SEQUENCE: 19

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<210> SEQ ID NO 20
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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 20

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attacgaccc aaataaatgc actgtgttagt gtgtcacag ggctccgggg cctttcgaaa	180
ggttctctgt ttgcttttg	199

We claim:

1. A method for identifying a sample as containing or not containing a vaginal epithelial cell, the method comprising the steps of:

(a) determining the level of methylation at the genetic locus of SEQ ID NO: 1 in:

i) a genomic DNA isolated from the sample, and
ii) optionally, a control genomic DNA;

(b) optionally, obtaining one or more reference values corresponding to the level of methylation at the genetic locus of SEQ ID NO: 1; and

(c) identifying the sample as containing, or not containing, the vaginal epithelial cell based on the level of

methylation at the genetic locus of SEQ ID NO: 1 in the genomic DNA isolated from the sample, wherein the level of methylation at the genetic locus of SEQ ID NO: 1 in the genomic DNA obtained from the sample is determined by high-resolution melt (HRM) analysis, wherein HRM comprises the steps of:
i) isolating the genomic DNA from the sample and optionally, the control sample;
ii) treating the isolated genomic DNA with bisulfite;
iii) polymerase chain reaction (PCR) amplifying the genetic locus of SEQ ID NO: 1 to produce the corresponding amplicon, wherein the PCR amplifying is performed using a primer pair comprising SEQ ID NOs: 2 and 3; and